

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=13; hr=15; min=10; sec=57; ms=260;
]

=====

Application No: 10813507 Version No: 3.0

Input Set:

Output Set:

Started: 2007-11-28 16:45:33.651
Finished: 2007-11-28 16:45:37.845
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 194 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> Lollar, John S.

<120> Nucleic Acid and Amino Acid Sequences
encoding High-Level Expressor Factor VIII Polypeptides and
Methods of Use

<130> 007157/ 276516

<140> 10813507

<141> 2004-03-30

<150> PCT/US02/33403

<151> 2002-10-07

<150> 60/327, 388

<151> 2001-10-05

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 6402

<212> DNA

<213> Sus scrofa

<220>

<221> gene

<222> (1)...(6399)

<223> Factor VIII-- Full Length

<221> CDS

<222> (1)...(6399)

<400> 1

atg cag cta gag ctc tcc acc tgt gtc ttt ctg tgt ctc ttg cca ctc 48

Met Gln Leu Glu Leu Ser Thr Cys Val Phe Leu Cys Leu Leu Pro Leu

1 5 10 15

ggc ttt agt gcc atc agg aga tac tac ctg ggc gca gtg gaa ctg tcc 96

Gly Phe Ser Ala Ile Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser

20 25 30

tgg gac tac cgg caa agt gaa ctc ctc cgt gag ctg cac gtg gac acc 144

Trp Asp Tyr Arg Gln Ser Glu Leu Leu Arg Glu Leu His Val Asp Thr

35 40 45

aga ttt cct gct aca gcg cca gga gct ctt ccg ttg ggc ccg tca gtc 192

Arg Phe Pro Ala Thr Ala Pro Gly Ala Leu Pro Leu Gly Pro Ser Val

50 55 60

ctg tac aaa aag act gtg ttc gta gag ttc acg gat caa ctt ttc agc 240

Leu Tyr Lys Lys Thr Val Phe Val Glu Phe Thr Asp Gln Leu Phe Ser

65 70 75 80

gtt gcc agg ccc agg cca cca tgg atg ggt ctg ctg ggt cct acc atc			288
Val Ala Arg Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile			
85	90	95	
cag gct gag gtt tac gac acg gtg gtc gtt acc ctg aag aac atg gct			336
Gln Ala Glu Val Tyr Asp Thr Val Val Val Thr Leu Lys Asn Met Ala			
100	105	110	
tct cat ccc gtt agt ctt cac gct gtc ggc gtc tcc ttc tgg aaa tct			384
Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Phe Trp Lys Ser			
115	120	125	
tcc gaa ggc gct gaa tat gag gat cac acc agc caa agg gag aag gaa			432
Ser Glu Gly Ala Glu Tyr Glu Asp His Thr Ser Gln Arg Glu Lys Glu			
130	135	140	
gac gat aaa gtc ctt ccc ggt aaa agc caa acc tac gtc tgg cag gtc			480
Asp Asp Lys Val Leu Pro Gly Lys Ser Gln Thr Tyr Val Trp Gln Val			
145	150	155	160
ctg aaa gaa aat ggt cca aca gca tct gac cca cca tgt ctc acc tac			528
Leu Lys Glu Asn Gly Pro Thr Ala Ser Asp Pro Pro Cys Leu Thr Tyr			
165	170	175	
tca tac ctg tct cac gtg gac ctg gtg aaa gac ctg aat tcg ggc ctc			576
Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu			
180	185	190	
att gga gcc ctg ctg gtt tgt aga gaa ggg agt ctg acc aga gaa agg			624
Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Thr Arg Glu Arg			
195	200	205	
acc cag aac ctg cac gaa ttt gta cta ctt ttt gct gtc ttt gat gaa			672
Thr Gln Asn Leu His Glu Phe Val Leu Leu Phe Ala Val Phe Asp Glu			
210	215	220	
ggg aaa agt tgg cac tca gca aga aat gac tcc tgg aca cgg gcc atg			720
Gly Lys Ser Trp His Ser Ala Arg Asn Asp Ser Trp Thr Arg Ala Met			
225	230	235	240
gat ccc gca cct gcc agg gcc cag cct gca atg cac aca gtc aat ggc			768
Asp Pro Ala Pro Ala Arg Ala Gln Pro Ala Met His Thr Val Asn Gly			
245	250	255	
tat gtc aac agg tct ctg cca ggt ctg atc gga tgt cat aag aaa tca			816
Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Lys Lys Ser			
260	265	270	
gtc tac tgg cac gtg att gga atg ggc acc agc ccg gaa gtg cac tcc			864
Val Tyr Trp His Val Ile Gly Met Gly Thr Ser Pro Glu Val His Ser			
275	280	285	
att ttt ctt gaa ggc cac acg ttt ctc gtg agg cac cat cgc cag gct			912
Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg His His Arg Gln Ala			
290	295	300	

tcc ttg gag atc tcg cca cta act ttc ctc act gct cag aca ttc ctg			960
Ser Leu Glu Ile Ser Pro Leu Thr Phe Leu Thr Ala Gln Thr Phe Leu			
305	310	315	320
atg gac ctt ggc cag ttc cta ctg ttt tgt cat atc tct tcc cac cac			1008
Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His His			
325	330	335	
cat ggt ggc atg gag gct cac gtc aga gta gaa agc tgc gcc gag gag			1056
His Gly Gly Met Glu Ala His Val Arg Val Glu Ser Cys Ala Glu Glu			
340	345	350	
ccc cag ctg cgg agg aaa gct gat gaa gag gaa gat tat gat gac aat			1104
Pro Gln Leu Arg Arg Lys Ala Asp Glu Glu Asp Tyr Asp Asp Asn			
355	360	365	
ttg tac gac tcg gac atg gac gtg gtc cgg ctc gat ggt gac gac gtg			1152
Leu Tyr Asp Ser Asp Met Asp Val Val Arg Leu Asp Gly Asp Asp Val			
370	375	380	
tct ccc ttt atc caa atc atc cgc tcg gtt gcc aag aag cat ccc aaa acc			1200
Ser Pro Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr			
385	390	395	400
tgg gtg cac tac atc tct gca gag gag gag gac tac gac gcc ccc			1248
Trp Val His Tyr Ile Ser Ala Glu Glu Asp Trp Asp Tyr Ala Pro			
405	410	415	
gcg gtc ccc agc ccc agt gac aga agt tat aaa agt ctc tac ttg aac			1296
Ala Val Pro Ser Pro Ser Asp Arg Ser Tyr Lys Ser Leu Tyr Leu Asn			
420	425	430	
agt ggt cct cag cga att ggt agg aaa tac aaa aaa gct cga ttc gtc			1344
Ser Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Ala Arg Phe Val			
435	440	445	
gct tac acg gat gta aca ttt aag act cgt aaa gct att ccg tat gaa			1392
Ala Tyr Thr Asp Val Thr Phe Lys Thr Arg Lys Ala Ile Pro Tyr Glu			
450	455	460	
tca gga atc ctg gga cct tta ctt tat gga gaa gtt gga gac aca ctt			1440
Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu			
465	470	475	480
ttg att ata ttt aag aat aaa gcg agc cga cca tat aac atc tac cct			1488
Leu Ile Ile Phe Lys Asn Lys Ala Ser Arg Pro Tyr Asn Ile Tyr Pro			
485	490	495	
cat gga atc act gat gtc agc gct ttg cac cca ggg aga ctt cta aaa			1536
His Gly Ile Thr Asp Val Ser Ala Leu His Pro Gly Arg Leu Leu Lys			
500	505	510	
ggt tgg aaa cat ttg aaa gac atg cca att ctg cca gga gag act ttc			1584
Gly Trp Lys His Leu Lys Asp Met Pro Ile Leu Pro Gly Glu Thr Phe			
515	520	525	
aag tat aaa tgg aca gtg act gtg gaa gat ggg cca acc aag tcc gat			1632

755	760	765	
agt gcg agc caa aag caa ttc caa acc atc aca agt cca gaa gat gac Ser Ala Ser Gln Lys Gln Phe Gln Thr Ile Thr Ser Pro Glu Asp Asp			2352
770	775	780	
gtg gag ctt gac ccg cag tct gga gag aga acc caa gca ctg gaa gaa Val Glu Leu Asp Pro Gln Ser Gly Glu Arg Thr Gln Ala Leu Glu Glu			2400
785	790	795	800
cta agt gtc ccc tct ggt gat ggg tcg atg ctc ttg gga cag aat cct Leu Ser Val Pro Ser Gly Asp Gly Ser Met Leu Leu Gly Gln Asn Pro			2448
805	810	815	
gct cca cat ggc tca tcc tca tct gat ctt caa gaa gcc agg aat gag Ala Pro His Gly Ser Ser Ser Asp Leu Gln Glu Ala Arg Asn Glu			2496
820	825	830	
gct gat gat tat tta cct gga gca aga gaa aga ggc acg gcc cca tcc Ala Asp Asp Tyr Leu Pro Gly Ala Arg Glu Arg Gly Thr Ala Pro Ser			2544
835	840	845	
gca gcg gca cgt ctc aga cca gag ctg cat cac agt gcc gaa aga gta Ala Ala Ala Arg Leu Arg Pro Glu Leu His His Ser Ala Glu Arg Val			2592
850	855	860	
ctt act cct gag cca gag aaa gag ttg aag aaa ctt gat tca aaa atg Leu Thr Pro Glu Pro Glu Lys Glu Leu Lys Lys Leu Asp Ser Lys Met			2640
865	870	875	880
tct agt tca tca gac ctt cta aag act tcg cca aca att cca tca gac Ser Ser Ser Asp Leu Leu Lys Thr Ser Pro Thr Ile Pro Ser Asp			2688
885	890	895	
acg ttg tca gcg gag act gaa agg aca cat tcc tta ggc ccc cca cac Thr Leu Ser Ala Glu Thr Glu Arg Thr His Ser Leu Gly Pro Pro His			2736
900	905	910	
ccg cag gtt aat ttc agg agt caa tta ggt gcc att gta ctt ggc aaa Pro Gln Val Asn Phe Arg Ser Gln Leu Gly Ala Ile Val Leu Gly Lys			2784
915	920	925	
aat tca tct cac ttt att ggg gct ggt gtc cct ttg ggc tcg act gag Asn Ser Ser His Phe Ile Gly Ala Gly Val Pro Leu Gly Ser Thr Glu			2832
930	935	940	
gag gat cat gaa agc tcc ctg gga gaa aat gta tca cca gtg gag agt Glu Asp His Glu Ser Ser Leu Gly Glu Asn Val Ser Pro Val Glu Ser			2880
945	950	955	960
gac ggg ata ttt gaa aag gaa aga gct cat gga cct gct tca ctg acc Asp Gly Ile Phe Glu Lys Glu Arg Ala His Gly Pro Ala Ser Leu Thr			2928
965	970	975	
aaa gac gat gtt tta ttt aaa gtt aat atc tct ttg gta aag aca aac Lys Asp Asp Val Leu Phe Lys Val Asn Ile Ser Leu Val Lys Thr Asn			2976
980	985	990	

aag gca cga gtt tac tta aaa act aat aga aag att cac att gat gac			3024
Lys Ala Arg Val Tyr Leu Lys Thr Asn Arg Lys Ile His Ile Asp Asp			
995	1000	1005	
 gca gct tta tta act gag aat agg gca tct gca acg ttt atg gac aaa			3072
Ala Ala Leu Leu Thr Glu Asn Arg Ala Ser Ala Thr Phe Met Asp Lys			
1010	1015	1020	
 aat act aca gct tcg gga tta aat cat gtg tca aat tgg ata aaa ggg			3120
Asn Thr Thr Ala Ser Gly Leu Asn His Val Ser Asn Trp Ile Lys Gly			
1025	1030	1035	1040
 ccc ctt ggc aag aac ccc cta agc tcg gag cga ggc ccc agt cca gag			3168
Pro Leu Gly Lys Asn Pro Leu Ser Ser Glu Arg Gly Pro Ser Pro Glu			
1045	1050	1055	
 ctt ctg aca tct tca gga tca gga aaa tct gtg aaa ggt cag agt tct			3216
Leu Leu Thr Ser Ser Gly Ser Gly Lys Ser Val Lys Gly Gln Ser Ser			
1060	1065	1070	
 ggg cag ggg aga ata cgg gtg gca gtg gaa gag gaa gaa ctg agc aaa			3264
Gly Gln Gly Arg Ile Arg Val Ala Val Glu Glu Glu Leu Ser Lys			
1075	1080	1085	
 ggc aaa gag atg atg ctt ccc aac agc gag ctc acc ttt ctc act aac			3312
Gly Lys Glu Met Met Leu Pro Asn Ser Glu Leu Thr Phe Leu Thr Asn			
1090	1095	1100	
 tcg gct gat gtc caa gga aac gat aca cac agt caa gga aaa aag tct			3360
Ser Ala Asp Val Gln Gly Asn Asp Thr His Ser Gln Gly Lys Lys Ser			
1105	1110	1115	1120
 cgg gaa gag atg gaa agg aga gaa aaa tta gtc caa gaa aaa gtc gac			3408
Arg Glu Glu Met Glu Arg Arg Glu Lys Leu Val Gln Glu Lys Val Asp			
1125	1130	1135	
 ttg cct cag gtg tat aca gcg act gga act aag aat ttc ctg aga aac			3456
Leu Pro Gln Val Tyr Thr Ala Thr Gly Thr Lys Asn Phe Leu Arg Asn			
1140	1145	1150	
 att ttt cac caa agc act gag ccc agt gta gaa ggg ttt gat ggg ggg			3504
Ile Phe His Gln Ser Thr Glu Pro Ser Val Glu Gly Phe Asp Gly Gly			
1155	1160	1165	
 tca cat gcg ccg gtg cct caa gac agc agg tca tta aat gat tcg gca			3552
Ser His Ala Pro Val Pro Gln Asp Ser Arg Ser Leu Asn Asp Ser Ala			
1170	1175	1180	
 gag aga gca gag act cac ata gcc cat ttc tca gca att agg gaa gag			3600
Glu Arg Ala Glu Thr His Ile Ala His Phe Ser Ala Ile Arg Glu Glu			
1185	1190	1195	1200
 gca ccc ttg gaa gcc ccg gga aat cga aca ggt cca ggt ccg agg agt			3648
Ala Pro Leu Glu Ala Pro Gly Asn Arg Thr Gly Pro Gly Pro Arg Ser			
1205	1210	1215	

gcg gtt ccc cgc cgc gtt aag cag agc ttg aaa cag atc aga ctc ccg Ala Val Pro Arg Arg Val Lys Gln Ser Leu Lys Gln Ile Arg Leu Pro	1220	1225	1230	3696	
cta gaa gaa ata aag cct gaa agg ggg gtg gtt ctg aat gcc acc tca Leu Glu Glu Ile Lys Pro Glu Arg Gly Val Val Leu Asn Ala Thr Ser	1235	1240	1245	3744	
acc cgg tgg tct gaa agc agt cct atc tta caa gga gcc aaa aga aat Thr Arg Trp Ser Glu Ser Ser Pro Ile Leu Gln Gly Ala Lys Arg Asn	1250	1255	1260	3792	
aac ctt tct tta cct ttc ctg acc ttg gaa atg gcc gga ggt caa gga Asn Leu Ser Leu Pro Phe Leu Thr Leu Glu Met Ala Gly Gly Gln Gly	1265	1270	1275	1280	3840
aag atc agc gcc ctg ggg aaa agt gcc gca ggc ccg ctg gcg tcc ggg Lys Ile Ser Ala Leu Gly Lys Ser Ala Ala Gly Pro Leu Ala Ser Gly	1285	1290	1295	3888	
aag ctg gag aag gct gtt ctc tct tca gca ggc ttg tct gaa gca tct Lys Leu Glu Lys Ala Val Leu Ser Ser Ala Gly Leu Ser Glu Ala Ser	1300	1305	1310	3936	
ggc aaa gct gag ttt ctt cct aaa gtt cga gtt cat cgg gaa gac ctg Gly Lys Ala Glu Phe Leu Pro Lys Val Arg Val His Arg Glu Asp Leu	1315	1320	1325	3984	
ttg cct caa aaa acc agc aat gtt tct tgc gca cac ggg gat ctc ggc Leu Pro Gln Lys Thr Ser Asn Val Ser Cys Ala His Gly Asp Leu Gly	1330	1335	1340	4032	
cag gag atc ttc ctg cag aaa aca cgg gga cct gtt aac ctg aac aaa Gln Glu Ile Phe Leu Gln Lys Thr Arg Gly Pro Val Asn Leu Asn Lys	1345	1350	1355	1360	4080
gta aat aga cct gga agg act ccc tcc aag ctt ctg ggt ccc ccg atg Val Asn Arg Pro Gly Arg Thr Pro Ser Lys Leu Leu Gly Pro Pro Met	1365	1370	1375	4128	
ccc aaa gag tgg gaa tcc cta gag aag tca cca aaa agc aca gct ctc Pro Lys Glu Trp Glu Ser Leu Glu Lys Ser Pro Lys Ser Thr Ala Leu	1380	1385	1390	4176	
agg acg aaa gac atc atc agt tta ccc ctg gac cgt cac gaa agc aat				4224	